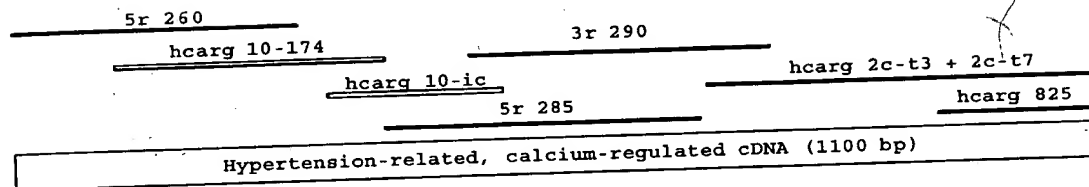


A



B

-131

GTAAAGGCTTGGTTTGTATTGTAAATGCAACTGTGGTTAGGACCTTCTCTTCGGACTGGTCAAGAAACGGGAAGAAAGG -80
 ATG TCT GCT TTG GGG GCT GCA GCT CCA TAC TTG CAC CAT CCC GCT GAC AGT CAC AGT GGC -1
 Met Ser Ala Leu Gly Ala Ala Pro Tyr Leu His His Pro Ala Asp Ser His Ser Gly 60
 CGG GTC AGT TTC CTG GGT TCC CAG CCC TCT CCA GAA GTG ACG GCC GTG GCT CAG CTC TTG 120
 Arg Val Ser Phe Leu Gly Ser Gln Pro Ser Pro Glu Val Thr Ala Val Ala Gln Leu Leu
 AAG GAC TTA GAC AGG AGC ACC TTC AGA AAG TTG TTG AAA CTT GTA GTC GGG GCC CTG CAT 180
 Lys Asp Leu Asp Arg Ser Thr Phe Arg Lys Leu Leu Lys Leu Val Val Gly Ala Leu His
 GGG AAA GAC TGC AGA GAA GCT GTG GAG CAA CTT GGT GCC AGC GCC AAC CTG TCA GAA GAG 240
 Gly Lys Asp Cys Arg Glu Ala Val Glu Gln Leu Gly Ala Ser Ala Asn Leu Ser Glu Glu
 CGT CTG GCC GTC CTG CTG GCG GGC ACA CAC ACC CTG CTC CAG CAG GCT CTC CGG CTG CCC 300
 Arg Leu Ala Val Leu Leu Ala Gly Thr His Thr Leu Leu Gln Gln Ala Leu Arg Leu Pro
 CCT GCT AGT CTA AAG CCA GAT GCC TTC CAG GAA GAG CTC CAG GAA CTT GGC ATT CCT CAG 360
 Pro Ala Ser Leu Lys Pro Asp Ala Phe Gln Glu Glu Leu Gln Glu Leu Gly Ile Pro Gln
 GAT CTA ATT GGA GAT TTG GCC AGT TTG GCA TTT GGG AGT CAA CGC CCT CTT CTC GAC TCT 420
 Asp Leu Ile Gly Asp Leu Ala Ser Leu Ala Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser
 GTA GCC CAA CAG CAG GGA TCC TCG CTG CCT CAC GTG TCT TAC TTC CGG TGG CGG GTG GAC 480
 Val Ala Gln Gln Gln Gly Ser Ser Leu Pro His Val Ser Tyr Phe Arg Trp Arg Val Asp
 GTG GCC ATC TCA ACC AGC GCT CAG TCC CGC TCC CTG CAA CCG AGT GTT CTC ATG CAG CTG 540
 Val Ala Ile Ser Thr Ser Ala Gln Ser Arg Ser Leu Gln Pro Ser Val Leu Met Gln Leu
 AAG CTC ACA GAT GGA TCT GCA CAC CGC TTC GAG GTG CCC ATA GCC AAA TTT CAG GAG CTG 600
 Lys Leu Thr Asp Gly Ser Ala His Arg Phe Glu Val Pro Ile Ala Lys Phe Gln Glu Leu
 CGG TAC AGT GTA GCC TTG GTC CTT AAG GAG ATG GCA GAA CTG GAG AAG AAG TGT GAG CGC 660
 Arg Tyr Ser Val Ala Leu Val Leu Lys Glu Met Ala Glu Leu Lys Lys Cys Glu Arg
 AAA CTG CAG GAC TGA CTGAACCCTGGTACTGTGGGTGCTGAAGCTGGTACCAGAACACAGCCCCCACTGGTGA 734
 Lys Leu Gln Asp TER
 TGAGCCCAACTCCATTGAGGTCCTGCATGTGAGAACGTATTTTAAAGTGAAGACAGCGGACTTTCAGGTTTGTGTTT 813
 ATGAGTCAACAGCTGGGCAGGGTGGCACAGTTTATAATCTCAGCCCTTGAAGTCTGAGGCTGGAGAATGGGAAGTGTA 892
 AGCTGGGCCTGGCTTTCATAGTGAGGCTCAGTGTGCAATTAAAGAGGTAAAGCAACTATTAAAAAAAAAAAAAAAAAAAA 969

FIGURE 1

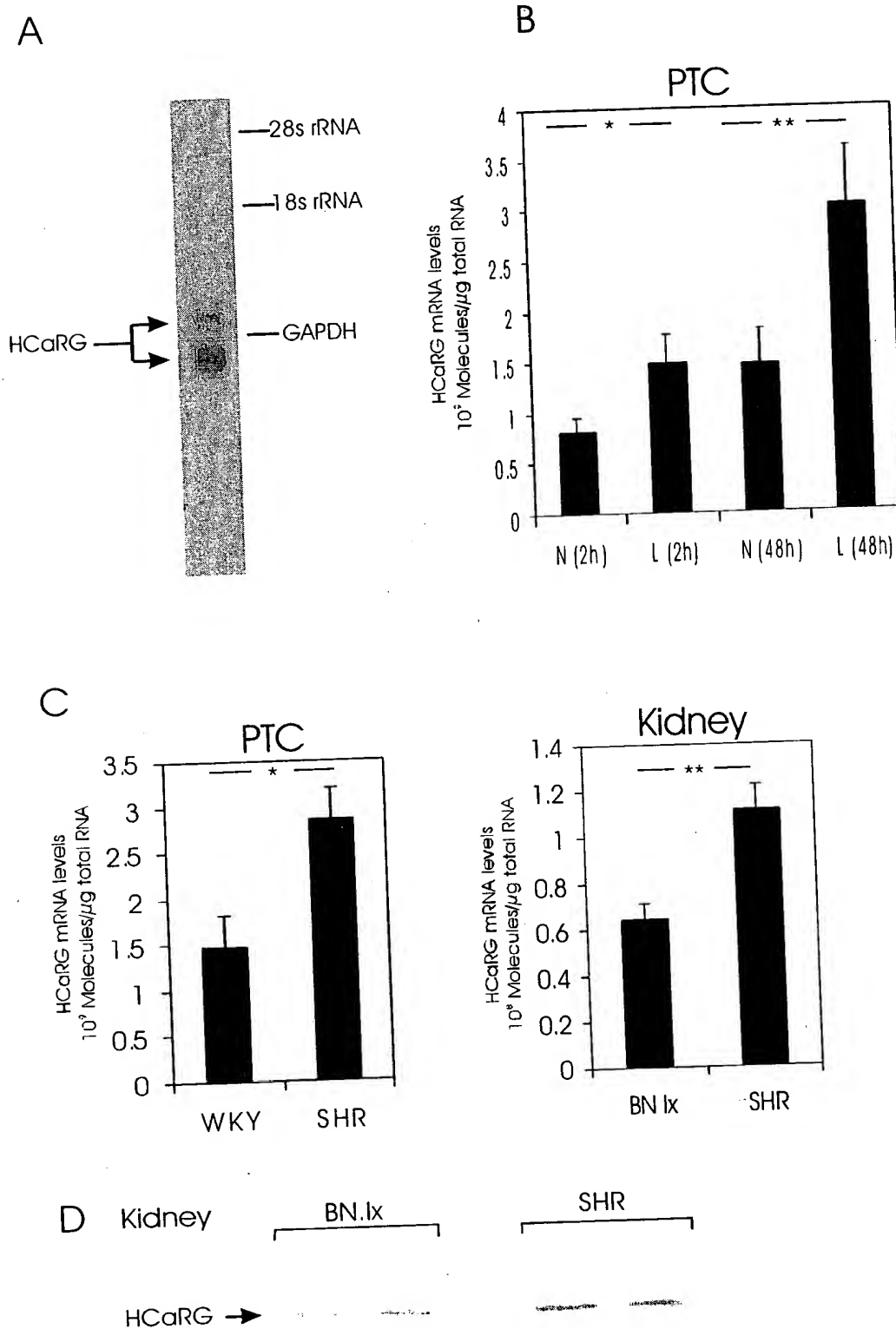


FIGURE 2

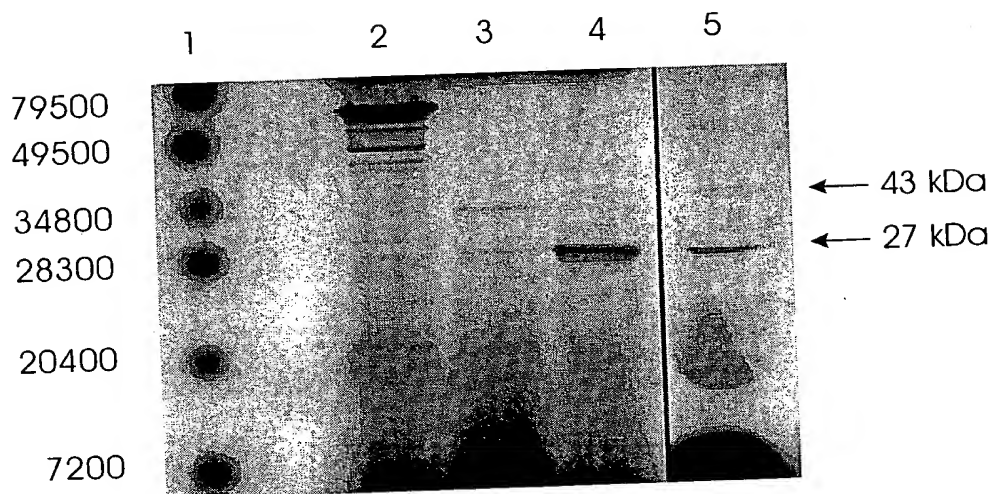


FIGURE 3

rHCaRG	MSAIGAAAPY LHHFADSHSG RVSFLGSQPS	PEVTIAMAQLL KDILDRSTFRK	50
hHCaRG	MSAVGAATPY LHHFGDSHSG RVSFLGAQLP	PEVAAMARLL GDILDRSTFRK	50
rHCaRG	LLKLVMGATH GKDCREAVEQ LGASANLSEE RLAVLLAGTH TLLOQALRLP		100
hHCaRG	LLKEFVSSIQ GEDCREAVQR LCVSANLPPE CLCALLAGMH TLLOQALRLP		100
rHCaRG	PASLKPDAFQ EELQELGIPQ DLTGDLASLA FGSQRPLLDS VAQQQGSSLP		150
hHCaRG	PTSLKPDIFR DQLQELGIPQ DLVGDLASVV FGSQRPLLDS VAQQQGAWLP		150
rHCaRG	HVSYFRWRVD VAISTSAQSR SLOPSVLMQL KLTGSAHRF EVETAKFQEL		200
hHCaRG	HVADFRWRVD VAISTSALAR SLOPSVLMQL KLSGSAYRF EVETAKFQEL		200
rHCaRG	RYSVALVLKE MAELEKKCER KLQD		224
hHCaRG	RYSVALVLKE MADLEKRCER RLQD		224

FIGURE 4

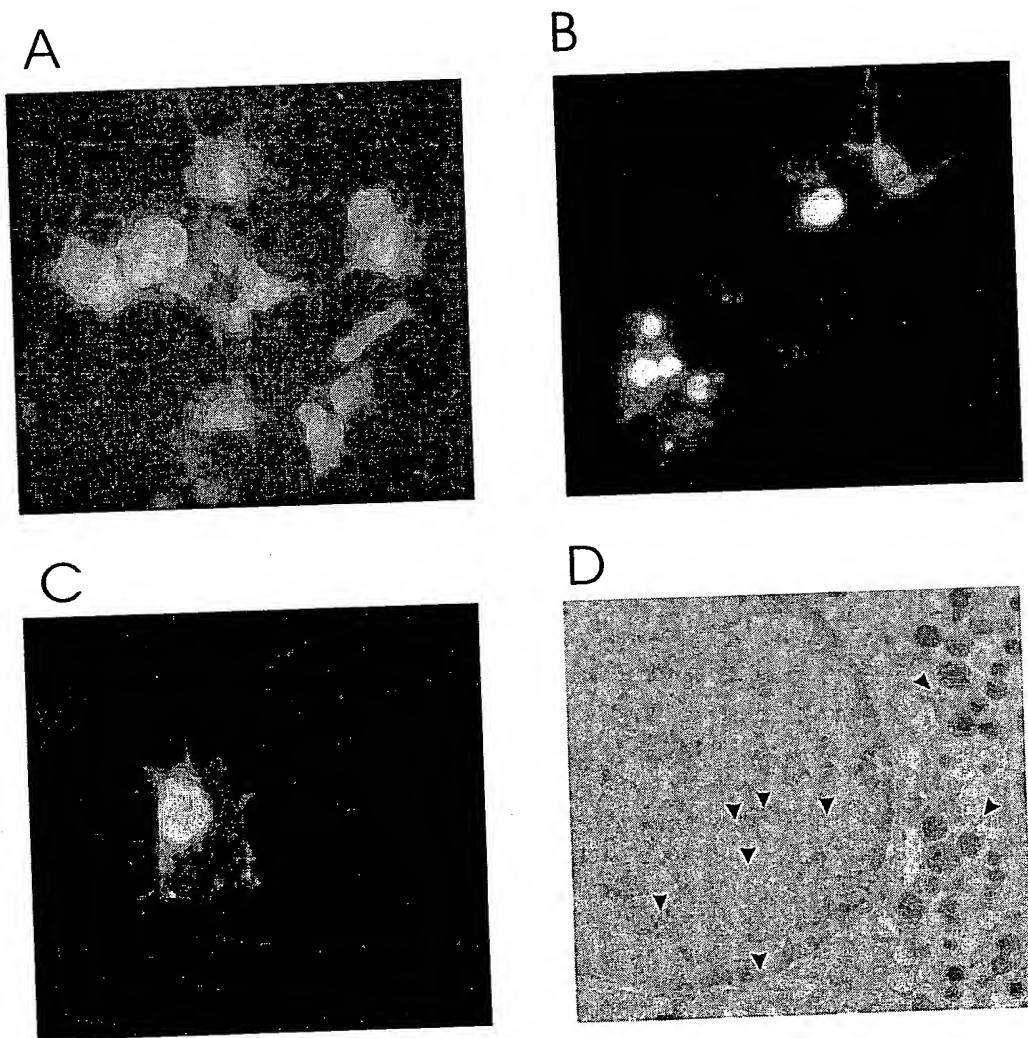
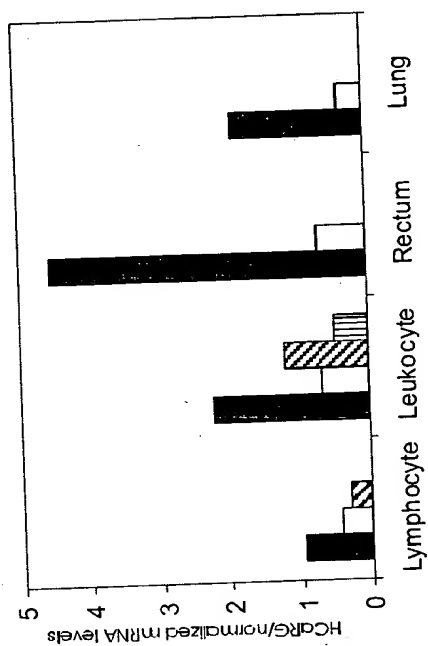
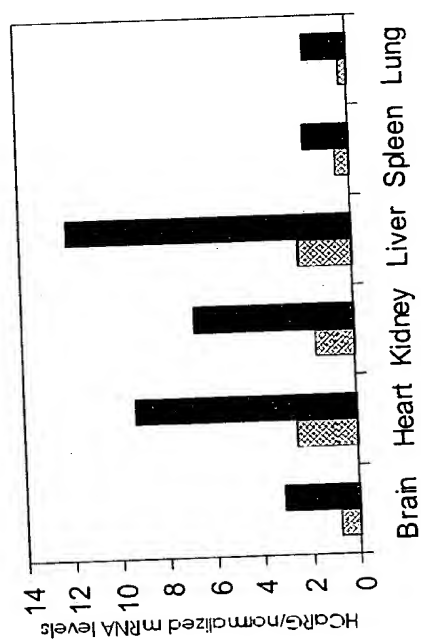


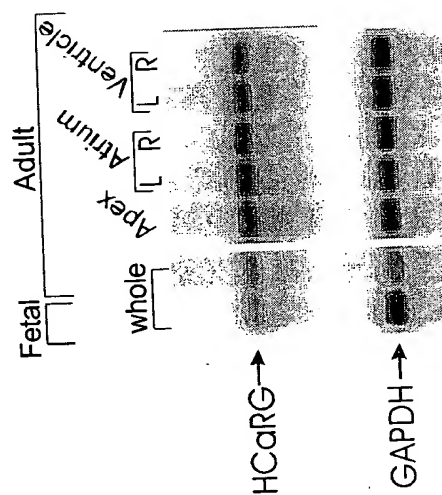
FIGURE 5

FIG 6: HCaRG mRNA expression in normal and cancerous tissues

A Fetal/Adult



B HEART



D Tumor/Normal

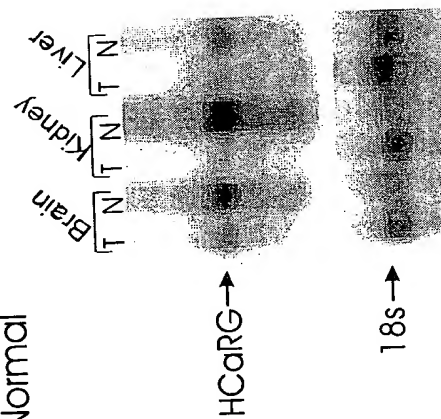


FIGURE 6

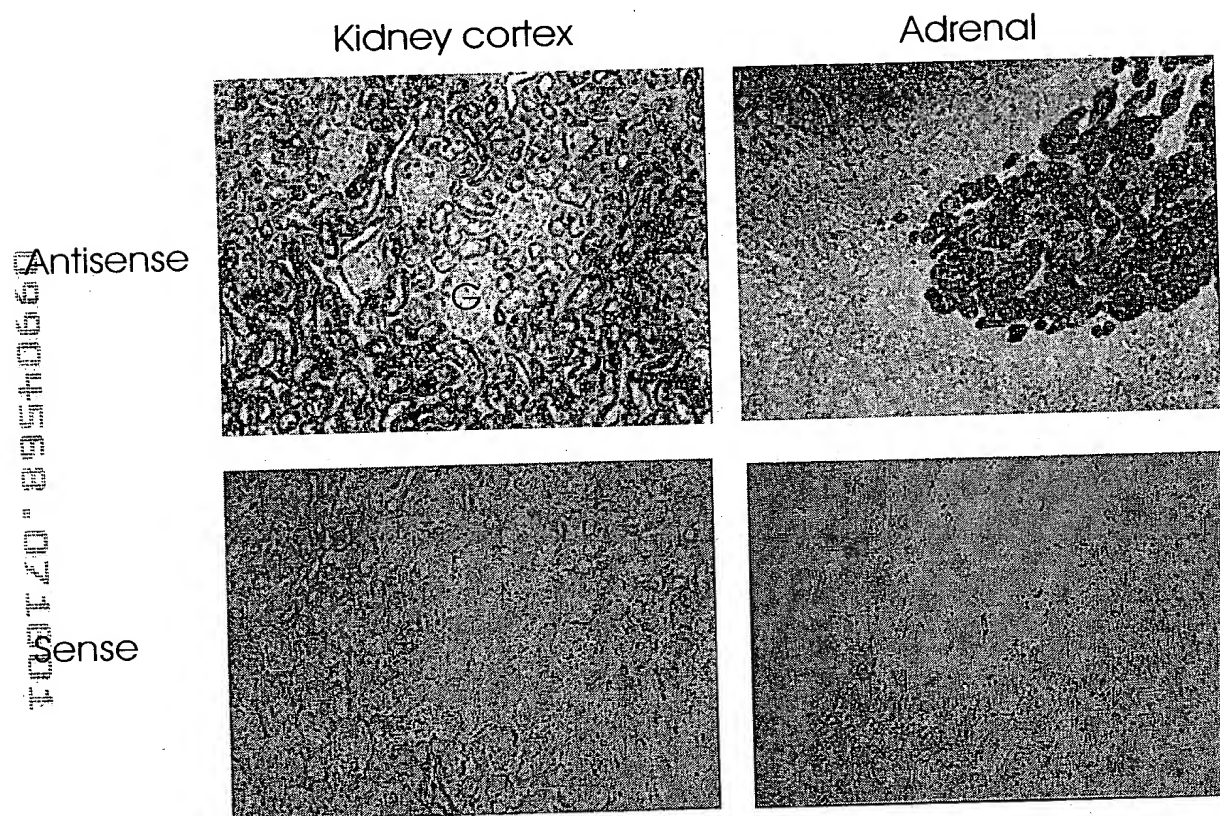
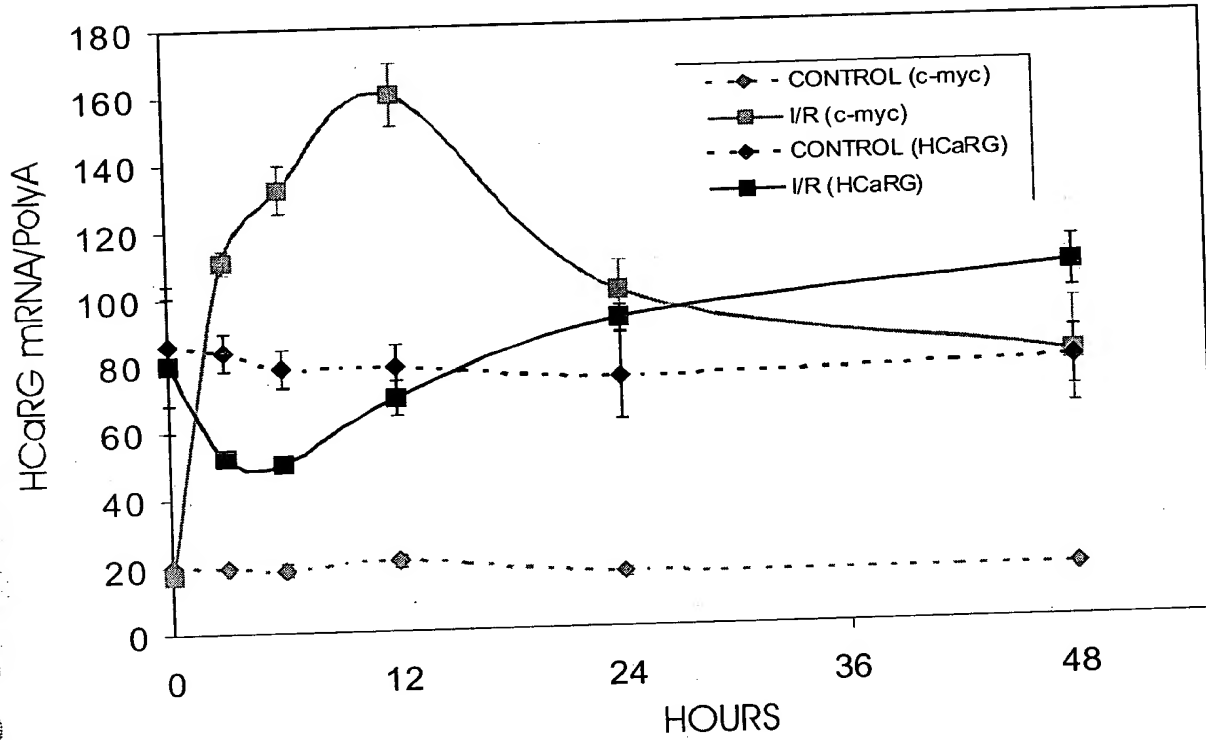
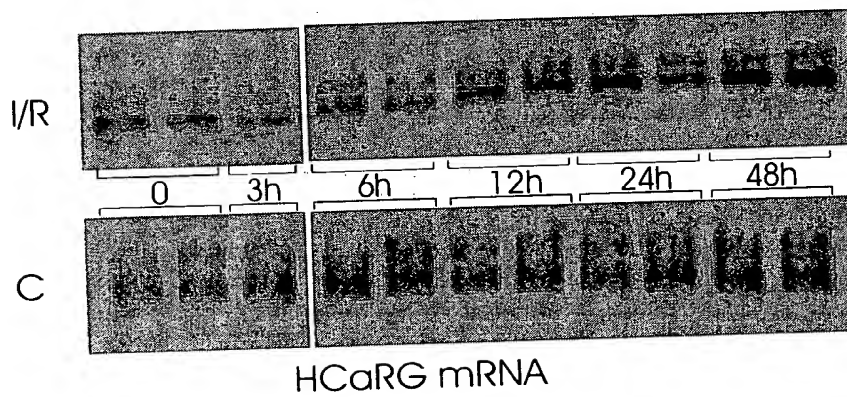


FIGURE 7

A Medulla



B Cortex



C Cortex

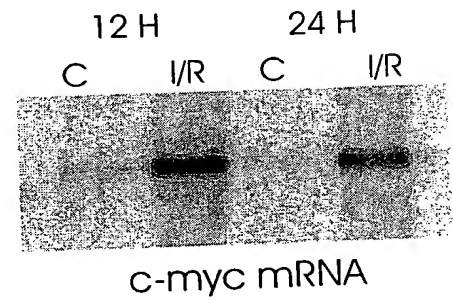
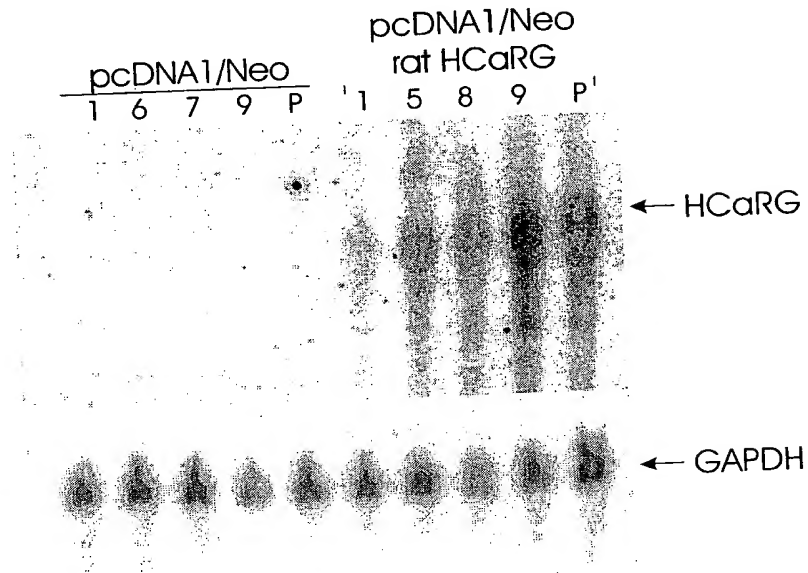


FIGURE 8

A



B

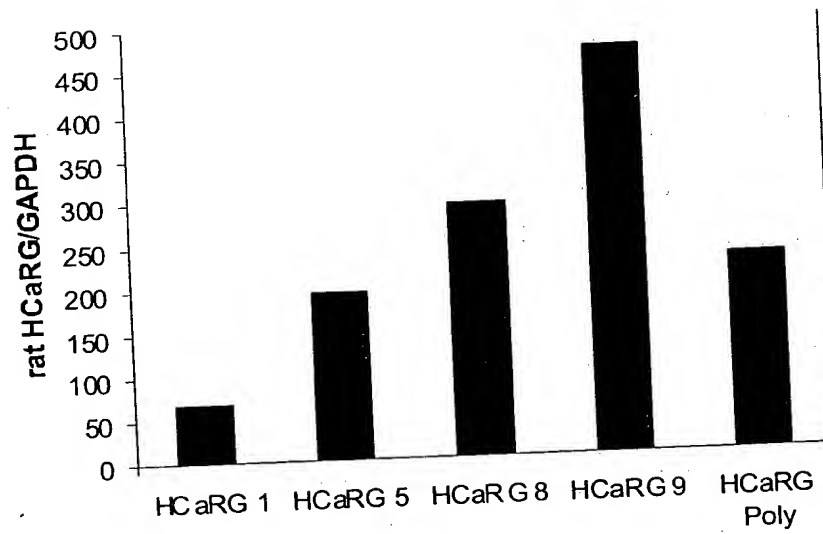
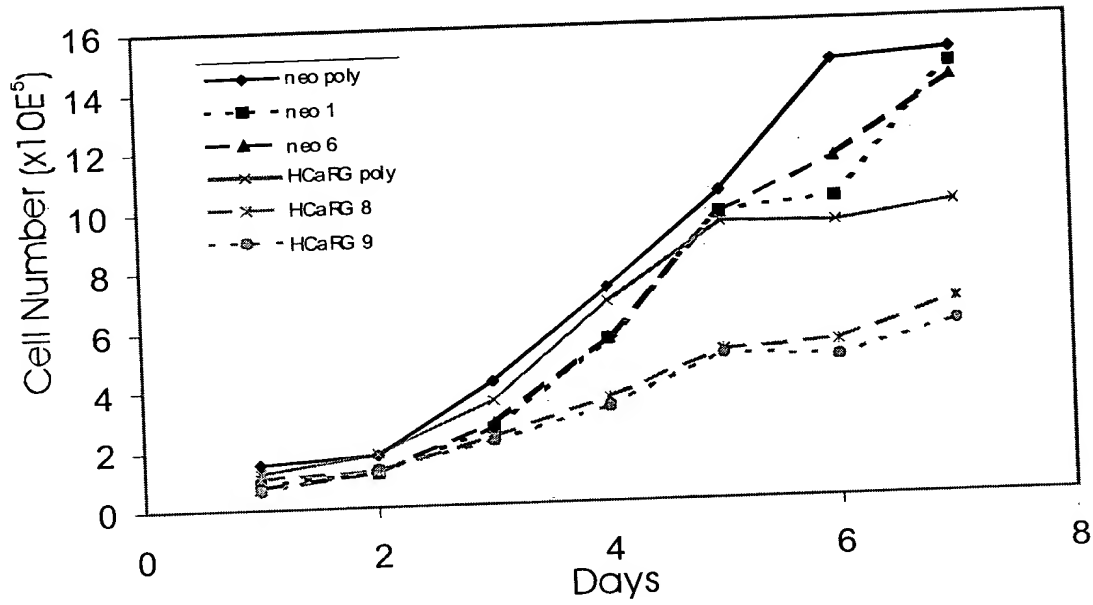


FIGURE 9

A



B

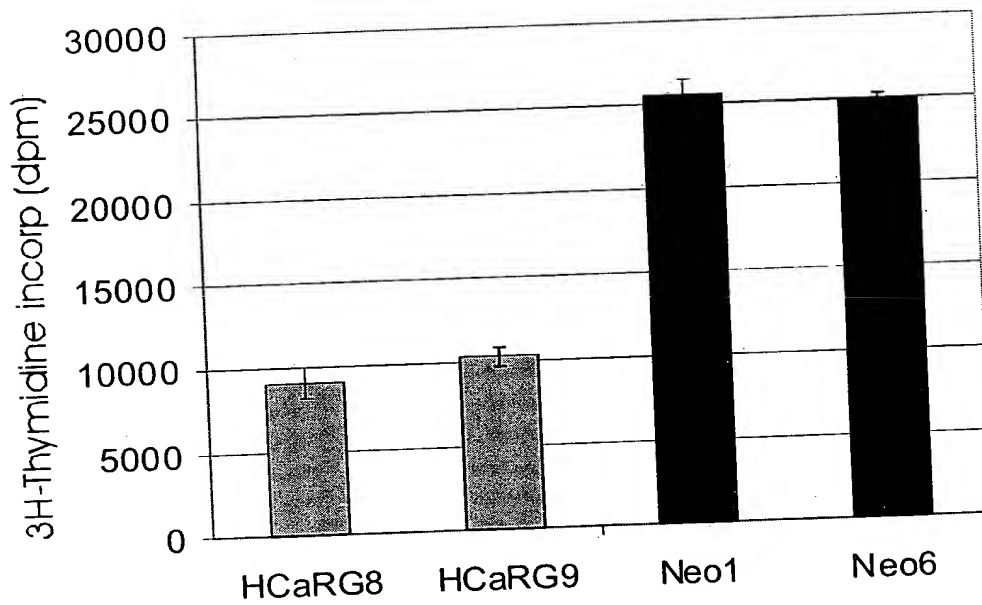


FIGURE 10

TOPF20" 89540660

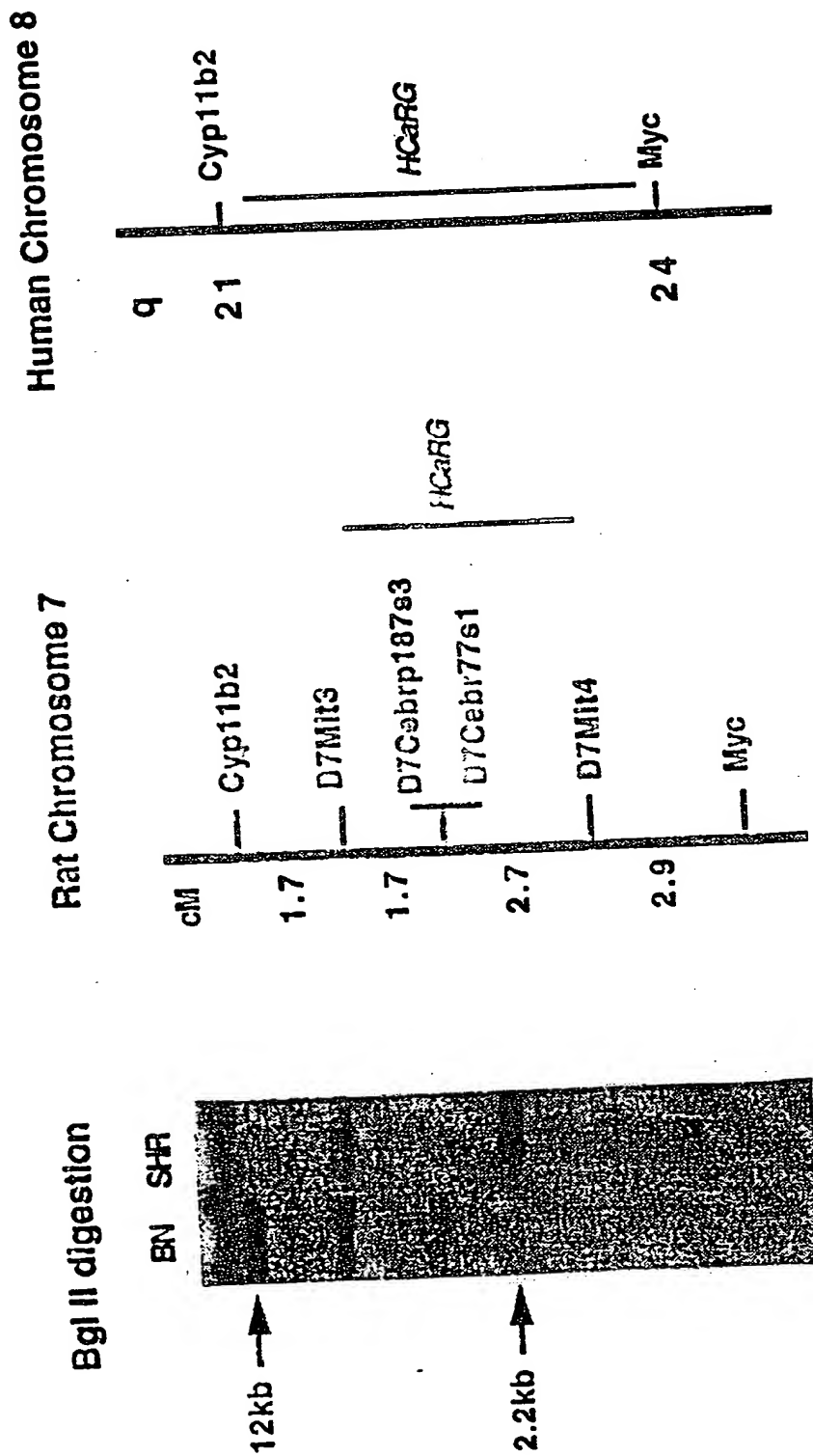


FIGURE 11